



RECEIVED

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Sequence Listing

<110> ASHKENAZI, AVI J  
BOTSTEIN, DAVID  
DODGE, KELLY H.  
GURNEY, AUSTIN L.  
KIM, KYUNG JIN  
LAWRENCE, DAVID A.  
PITTI, ROBERT  
ROY, MARGARET A  
TUMAS, DANIEL B  
WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289

<141> 1998-09-18

<150> US 60/059,288

<151> 1997-09-18

<150> US 60/094,640

<151> 1998-07-30

<160> 18

<210> 1

<211> 300

<212> PRT

<213> Homo sapiens

<400> 1

Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val  
1 5 10 15

Leu Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val  
20 25 30

Ala Glu Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu  
35 40 45

Arg Leu Val Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg  
50 55 60

Pro Cys Arg Arg Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro  
65 70 75

Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr  
80 85 90

Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu	Glu	Ala	Arg	Ala	Cys	95	100	105
His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg	Thr	Gly	Phe	Phe	110	115	120
Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys	Pro	Pro	Gly	125	130	135
Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr	Gln	Cys	140	145	150
Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser	155	160	165
Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala	170	175	180
Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser	185	190	195
Cys	Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu	200	205	210
Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser	215	220	225
Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu	230	235	240
Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu	245	250	255
Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly	260	265	270
Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met	275	280	285
Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His	290	295	300

<210> 2  
 <211> 1114  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> Unsure  
 <222> 1090

<223> Unknown base

<400> 2

tccgcaggcg gaccgggggc aaaggaggtg gcatgtcggc caggcacagc 50  
agggtcctgt gtccgcgctg agccgcgctc tccttgcctc agcaaggacc 100  
atgagggcgc tggaggggccc aggctgtcg ctgctgtgcc tgggtgttggc 150  
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200  
ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250  
cagtgcctcc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300  
cacgacgtgt ggcccgctc caccgcgcca ctacacgcag ttctggaact 350  
acctggagcg ctgccgctac tgcaacgtcc tctgcgggga gcgtgaggag 400  
gaggcacggg cttgccacgc caccacaaac cgtgcctgcc gctgccgcac 450  
cggcttcttc gcgcacgctg gtttctgctt ggagcacgca tcgtgtccac 500  
ctggtgccgg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550  
cagccgtgcc cccaggcac cttctcagcc agcagctcca gctcagagca 600  
gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650  
caggctcttc ctcccatgac accctgtgca ccagctgcac tggttcccc 700  
ctcagcacca ggggtaccag agctgaggag tgtgagcgtg ccgtcatoga 750  
ctttgtggct ttccaggaca tctccatcaa gaggtgcag cggctgctgc 800  
aggccctcga ggccccggag ggctggggtc cgacaccaag ggcgggccgc 850  
gcggccttgc agctgaagct gcgtcggcgg ctacaggagc tcctgggggc 900  
gcaggacggg gcgctgctgg tgccgctgct gcaggcgtg cgcgtggcca 950  
ggatgcccgg gctggagcgg agcgtccgtg agcgttctc cctgtgcac 1000  
tgatcctggc cccctcttat ttattctaca tccttggcac ccacttgca 1050  
ctgaaagagg ctttttttta aatagaagaa atgaggtttn ttaaaaaaaaa 1100  
aaaaaaaaaa aaaa 1114

<210> 3

<211> 491

<212> DNA  
<213> Unknown

<220>  
<223> Unknown organism

<220>  
<221> unsure  
<222> 62, 73, 86, 98  
<223> unknown base

<400> 3  
gccgagacag cccacgacg tgtggcccg gtccaccgc ccactacag 50  
cagttctgga antaactgga gcctgcccgc tactgnaacg tcctctgngg 100  
ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgcct 150  
gccgctgccg caccggcttc ttccgcacg ctggttttctg cttggagcac 200  
gcatcgtgtc cacctggtgc cggcgtgatt gccccgggca cccccagcca 250  
gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300  
tccagctcag agcagtgccg gccccaccgc aactgcacgg ccctgggcct 350  
ggccctcaat gtgccaggct cttcctccca tgacaccctg tgcaccagct 400  
gcactggctt cccctcagc accagggtag caggagctga ggagtgtgag 450  
cgtgcggtca tcgactttgt ggctttccag gacatctcca t 491

<210> 4  
<211> 73  
<212> DNA  
<213> Unknown

<220>  
<223> Unknown organism

<400> 4  
gccgagacag cccacgacg tgtggcccg gtccaccgc ccactacag 50  
cattctggaa ctacctggag cgc 73

<210> 5  
<211> 271  
<212> DNA  
<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

<223> unknown base

<400> 5

gccgagacag cccacgacg tgtggcccg gtccaccgc cnactacag 50

cagttctgga antaactgga gcnctgccgc tactgnaacg tcctctgngg 100

ggagcntgag gaggaggcan gngcttgcca cgccaccac aaccgcgcct 150

gcnctgcag caccggnctt ttcgcgcacg ctgntttctg cttggagcac 200

gcacgtgtc cacctggtgn cggcgtgatt gncccgggca cccccagcca 250

gaacacgcat gcaaagccgt g 271

<210> 6

<211> 201

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 182

<223> unknown base

<400> 6

gcagttctgg aactacctgg agcgtgccg ctactgcaac gtcctctgcg 50

gggagcgtga ggaggaggca cgggcttgcc acgccacca caaccgtgcc 100

tgccgctgcc gcaccggctt cttcgcgcac gctgggtttct gcttgagca 150

cgcacgtgt ccacctggtg cggcgtgat tnccccgggc acccccagcc 200

a 201

<210> 7

<211> 277

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 142

<223> unknown base

<400> 7

gaggggcccc caggagtggg ggccggaggt gtggcagggg tcaggttgct 50

ggtcccagcc ttgcacctg agctaggaca ccagttcccc tgacctgtt 100

cttcctcctt ggtgcaggc acccccagcc agaacacgca gnccagccgt 150

gccccccagg caccttctca gccagcagct ccagctcaga gcagtgccag 200

ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250

ttctcccat gacacctgt gcaccag 277

<210> 8

<211> 199

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 8

gcatcgtgtc cacctgggtg cggcgtgatt gccccgggca cccccagcca 50

gaacacgcag gcctagccgt gccccccagg caccttctca gccagcagct 100

ccagctcaga gcagtgccag cccccaccgca actgcacggc cctgggcctg 150

gccctcaatg tgccaggctc ttctcccat gacacctgt gcaccagct 199

<210> 9

<211> 226

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 4, 9, 12, 165

<223> unknown base

<400> 9

agcngtgcnc cncaggcacc ttctcagcca gcagttccag ctgagagcag 50

tgccagcccc accgcaactg cacggccctg ggcttgcccc tcaatgtgcc 100  
aggctcttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150  
tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcatcgac 200  
tttgtggctt tccaggacat ctccat 226

<210> 10  
<211> 283  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Unsure  
<222> 1-283  
<223> Unknown organism

<220>  
<221> unsure  
<222> 27, 64, 140  
<223> unknown base

<400> 10  
cttgtccacc tgggtgccggc gtgattnccc gggcaccccc agccagaaca 50  
cgcagtgcc a gcntcccc caggcacctt ctcagccagc agtccagct 100  
cagagcagtg ccagccccac cgcaactgca acgccctggn ctggccctca 150  
atgtgccagg ctcttctctcc catgacaccc tgtgcaccag ctgcactggc 200  
ttccccctca gcaccagggg accaggagct gaggagtgtg agcgtgccgt 250  
catcgacttt gtggctttcc aggacatctc cat 283

<210> 11  
<211> 21  
<212> DNA  
<213> Unknown

<220>  
<223> Unknown organism

<400> 11  
cacgctgggt tctgcttgga g 21

<210> 12  
<211> 22  
<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 12

agctggtgca caggggtgtca tg 22

<210> 13

<211> 53

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 13

cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag 50

ccc 53

<210> 14

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 14

acacgatgcg tgctccaagc agaa 24

<210> 15

<211> 17

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 15

cttcttcgcg cacgctg 17

<210> 16

<211> 16

<212> DNA

<213> Unknown

<220>

<223> Unknown organism



<400> 16  
atcacgccgg caccag 16

<210> 17  
<211> 461  
<212> PRT  
<213> Homo sapiens

<400> 17  
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu  
1 5 10 15  
Leu Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr  
20 25 30  
Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr  
35 40 45  
Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly  
50 55 60  
Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys  
65 70 75  
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val  
80 85 90  
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val  
95 100 105  
Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys  
110 115 120  
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg  
125 130 135  
Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala  
140 145 150  
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala  
155 160 165  
Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg  
170 175 180  
Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser  
185 190 195  
Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala  
200 205 210

Pro Gly Ala Val	His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln	215	220	225
His Thr Gln Pro	Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser	230	235	240
Phe Leu Leu Pro	Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr	245	250	255
Gly Asp Phe Ala	Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala	260	265	270
Leu Gly Leu Leu	Ile Ile Gly Val Val Asn Cys Val Ile Met Thr	275	280	285
Gln Val Lys Lys	Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val	290	295	300
Pro His Leu Pro	Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu	305	310	315
Gln Gln His Leu	Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser	320	325	330
Leu Glu Ser Ser	Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg	335	340	345
Asn Gln Pro Gln	Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu	350	355	360
Ala Arg Ala Ser	Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His	365	370	375
Gly Thr Gln Val	Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser	380	385	390
Ser Asp His Ser	Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met	395	400	405
Gly Asp Thr Asp	Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln	410	415	420
Val Pro Phe Ser	Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu	425	430	435
Thr Pro Glu Thr	Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro	440	445	450
Leu Gly Val Pro	Asp Ala Gly Met Lys Pro Ser	455	460	

<210> 18  
 <211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser
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Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His
				20					25					30
Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro
				35					40					45
Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr
				50					55					60
Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His
				65					70					75
Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu
				80					85					90
Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys
				95					100					105
Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys
				110					115					120
His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr
				125					130					135
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe
				140					145					150
Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn
				155					160					165
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr
				170					175					180
His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys
				185					190					195
Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala
				200					205					210
Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp
				215					220					225

Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys  
245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile  
260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile  
275 280 285

Gly His Ala Asn Leu Thr Phe Glu  
290